

Query Match 71.8%; Score 7756.5; DB 1; Length 1569;
 Best Local Similarity 93.1%; Pred. No. 0;
 Matches 1553; Conservative 1; Mismatches 1; Indels 113; Gaps 3;

QY 1 MTSIAQOQIQRALPOSDBSLSDREVASLFLDPKRAATIDDDAFATICTGTELLGIDP 60
 DB 2 MTSIAQOQIQRALPOSDBSLSDREVASLFLDPKRAATIDDDAFATICTGTELLGIDP 61

QY 61 SFEQEPAPLFSQAKTLERSVOTKAVNKQDENSILFLIHSPTFLKPAQCLEMLIHR 120
 DB 62 SFEQEPAPLFSQAKTLERSVOTKAVNKQDENSILFLIHSPTFLKPAQCLEMLIHR 121

QY 121 FHIHLYNODSLIACVLPYHETRIEVRVITQLKINNSKHEMFLPVKQGVPLAKGTLIT 180
 DB 122 FHIHLYNODSLIACVLPYHETRIEVRVITQLKINNSKHEMFLPVKQGVPLAKGTLIT 181

QY 181 HCYKDLGFMDFICSLNRSVAFAPYSSAQLVLAFASTVSAVAEDVSDNTIA 240
 DB 182 HCYKDLGFMDFICSLNRSVAFAPYSSAQLVLAFASTVSAVAEDVSDNTIA 241

QY 241 KLFPIYIGKGLKSLPDYRAATYMTICQISVRYTMENTFVNSLASQIITKTKIPSLIKDG 300
 DB 242 KLFPIYIGKGLKSLPDYRAATYMTICQISVRYTMENTFVNSLASQIITKTKIPSLIKDG 301

QY 301 LSCILVILQKRPESLQK-----PPHLCNVPDLITTLHGISETYDVSPSL 347
 DB 302 LSCILVILQKRPESLQKVVOLILRNGASQRPPLHCNVPDLITTLHGISETYDVSPSL 361

QY 348 RYMLPHLVASIIHVTGEGMDQIYKRLHLEILTKISIKNNLDHLASLEETYSY 407
 DB 362 HYMLPHLVASIIHVTGEGMDQIYKRLHLEILTKISIKNNLDHLASLEETYSY 421

QY 408 SSOEEMSNKVSLLNEQFLPLRLLESKYPTLDVLEEHLEKEIADLKQKLEFQFYSLS 467
 DB 422 SSOEEMSNKVSLLNEQFLPLRLLESKYPTLDVLEEHLEKEIADLKQKLEFQFYSLS 481

QY 468 TSGKTYOFLADSDTSLMSLNHPILAPVILAMNLKIKMTSKGVDSPTKEAVLARLG 527
 DB 482 TSGKTYO-----GVDSEPTKEAVLARLG 505

QY 528 DDNDIVVLSAISAEIFEKHEHSEVITISNLLNLFQRAELSKNGEMVYLKIAADILKEE 587
 DB 506 DDNDIVVLSAISAEIFEKHEHSEVITISNLLNLFQRAELSKNGEMVYLKIAADILKEE 565

QY 588 ILSNDOLSNQVVCLLPFPVYINNDTESAEMKTAIYLSKSGICSLPHLLRGMEALENV 647
 DB 566 ILSNDOLSNQVVCLLPFPVYINNDTESAEMKTAIYLSKSGICSLPHLLRGMEALENV 625

QY 648 IKSTRPKGLGVANOKMIELLADININGDSSMLKMWEDLISGEESEFNLKOKVTFHVI 707
 DB 626 IKSTRPKGLGVANOKMIELLADININGDSSMLKMWEDLISGEESEFNLKOKVTFHVI 661

QY 708 LSVLVSCSSSLKETHFPFAIRVFSLOKIKKLESVITAVEIPESEHIELMDRGIPVEL 767
 DB 662 -----EISESEHIELMDRGIPVEL 681

QY 768 WAHYVEELNSTQRAVAVDSVFLVFSLKKFYIALKAPKSPFKGDIWMNPQOLKEDSRDYLA 827
 DB 682 WAHYVEELNSTQRAVAVDSVFLVFSLKKFYIALKAPKSPFKGDIWMNPQOLKEDSRDYLA 741

QY 828 LLLGLFEMMLNGADAVHFRILMKLEIVHLEEDVOLFQKPCSVLMTYSSISNPLNCVKT 887
 DB 742 LLLGLFEMMLNGADAVHFRILMKLEIVHLEEDVOLFQKPCSVLMTYSSISNPLNCVKT 801

QY 888 VLQTOALYVCAMLSQKTOCKHQOLASISSPVYTSLLINLSGSPVKEVRAAIOCLALSG 947
 DB 802 VLQTOALYVCAMLSQKTOCKHQOLASISSPVYTSLLINLSGSPVKEVRAAIOCLALSG 861

QY 948 VASPEFYIIDLHLSKAETISDAAYVYQDILATFEELQKREKKLKHOKISETLKNLSCV 1007
 DB 862 VASPEFYIIDLHLSKAETISDAAYVYQDILATFEELQKREKKLKHOKISETLKNLSCV 921

QY 1008 YSCPSYIAKDLMLKVLQGVNGEMVLSOLLPMABOELLEKIOKEPTAVLKDEAMVHLTLGKY 1067
 DB 922 YSCPSYIAKDLMLKVLQGVNGEMVLSOLLPMABOELLEKIOKEPTAVLKDEAMVHLTLGKY 981

QY 1068 NEFSVSLNEDPKSLDIFIAVHTTKELVAGMPTIOITALEKITKPPFAAISDEKVOOKL 1127
 DB 982 NEFSVSLNEDPKSLDIFIAVHTTKELVAGMPTIOITALEKITKPPFAAISDEKVOOKL 1041

QY 1128 LRMLFDLLVNCNKHCHQOTVSSVFKGISVNAEOVRIELEPPDKAKPLGTVQOKRRQMOQ 1187
 DB 1042 LRMLFDLLVNCNKHCHQOTVSSVFKGISVNAEOVRIELEPPDKAKPLGTVQOKRRQMOQ 1101

QY 1188 KKSODLESVOEGSYQORVTLLELLOHKKLRSPOILVPTLFNLSCRLEPLPOEOGN 1247
 DB 1102 KKSODLESVOEGSYQORVTLLELLOHKKLRSPOILVPTLFNLSCRLEPLPOEOGN 1161

QY 1248 MEYTKQILSLCLNICOKLSPDGKIPKDLIDEEKFVVELIVOCIRLSEMPOTHHALLL 1307
 DB 1162 MEYTKQILSLCLNICOKLSPDGKIPKDLIDEEKFVVELIVOCIRLSEMPOTHHALLL 1221

QY 1308 LGTYAGIFPPKVLNHNISITFGANAMRLDDTYSFQVINKTVKAVIPALIQSDGDSIE 1367
 DB 1222 LGTYAGIFPPKVLNHNISITFGANAMRLDDTYSFQVINKTVKAVIPALIQSDGDSIE 1281

QY 1368 VSRNVEIIVKIIISVFDALPHVPEHRRPLIVOLVDTGAEEKFIMTLILFEQVYTKT 1427
 DB 1282 VSRNVEIIVKIIISVFDALPHVPEHRRPLIVOLVDTGAEEKFIMTLILFEQVYTKT 1341

QY 1428 VLAANGKDAILEADTEFWFVSCCEFSVOHQIOSLMLNLOYLKLPKEKEETIPRAVSF 1487
 DB 1342 VLAANGKDAILEADTEFWFVSCCEFSVOHQIOSLMLNLOYLKLPKEKEETIPRAVSF 1401

QY 1488 NKSSEMEMQVFNVEHNSKOLRHRKFLSVSPMSQSLSSNNFLKAVVSGEPILLKLE 1547
 DB 1402 NKSSEMEMQVFNVEHNSKOLRHRKFLSVSPMSQSLSSNNFLKAVVSGEPILLKLE 1461

QY 1548 ERLEETVLGYISAAVQSMERNADKLTVEFWRALLSKAYDLDBVNNLLPTEPIPIVIRGL 1607
 DB 1462 ERLEETVLGYISAAVQSMERNADKLTVEFWRALLSKAYDLDBVNNLLPTEPIPIVIRGL 1521

QY 1608 VGNPLDSVRRKALDLNNKLOONISMKKTIIVREKLVPDLIAIVORK 1655
 DB 1522 VGNPLDSVRRKALDLNNKLOONISMKKTIIVREKLVPDLIAIVORK 1569

RESULT 5
 US-08-936-487-52
 Sequence 52, Application US/08936487
 GENERAL INFORMATION:
 APPLICANT: Bowcock, Anne M.
 TITLE OF INVENTION: Compositions and Methods Comprising
 TITLE OF INVENTION: BARD1 and Other Brcal Binding Proteins
 NUMBER OF SEQUENCES: 130
 CORRESPONDENCE ADDRESS:
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/936.487
 FILING DATE: - Concurrently Herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/025.296

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; FILING DATE: 20-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,611
; FILING DATE: 03-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,985
; FILING DATE: 04-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: P-41,071
; REFERENCE/DOCKET NUMBER: UTSID:499
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-936-487-52

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Query Match      23.9% Score 2586; DB 13; Length 515;
Best Local Similarity 99.0%; Pred. No. 1.2e-197;
Matches 510; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 1630 NISMKTIYTRFLKLVDPDLAIYORRKGEGEOAIRGTALYTLKLCKNGAENPDF 1689
DB 1 NISMKTIYTRFLKLVDPDLAIYORRKGEGEOAIRGTALYTLKLCKNGAENPDF 60
QY 1690 VPLVTAIVKLIAPERKEENKVGSLICIAEYTSLEALAIPOLEPSMLTMTKNTSE 1749
DB 61 VPLVTAIVKLIAPERKEENKVGSLICIAEYTSLEALAIPOLEPSMLTMTKNTSE 120
QY 1750 LVSEVEYLLSALAALQKVEYLPHEFISPYLEGISQVHLEKITSMSGASQANIRLISL 1809
DB 121 LVSEVEYLLSALAALQKVEYLPHEFISPYLEGISQVHLEKITSMSGASQANIRLISL 180
QY 1810 KRLATTLAPRVLIPIAKTKYKQIEKNMKNHMGPPMSIIQEHIGAKKKEELTSHOSQLTA 1869
DB 181 KRLATTLAPRVLIPIAKTKYKQIEKNMKNHMGPPMSIIQEHIGAKKKEELTSHOSQLTA 240
QY 1870 FPLEALDFAHSENDLEEVGKTEKNCIIDCLVAMVYKLSSEVFRPLFEFLPMKTEDAP 1929
DB 241 FPLEALDFAHSENDLEEVGKTEKNCIIDCLVAMVYKLSSEVFRPLFEFLPMKTEDAP 300
QY 1930 KORLLTFYMLADCIAREKLGFTLFAHGLVKPFADTLXOVNISKTDEAFDSENDPEKCC 1989
DB 301 KORLLTFYMLADCIAREKLGFTLFAHGLVKPFADTLXOVNISKTDEAFDSENDPEKCC 360
QY 1990 LLLQFLINLKYKFLPDTHFISKERAKXALMPLVQLEENRIGEGEKFOEDRYTKHLIPCI 2049
DB 361 LLLQFLINLKYKFLPDTHFISKERAKXALMPLVQLEENRIGEGEKFOEDRYTKHLIPCI 420
QY 2050 AFEVSAMADDSLMKPLNYOILKTRDSSPKVRFALITVALAEKIKENVYLLPESIPF 2109
DB 421 AFEVSAMADDSLMKPLNYOILKTRDSSPKVRFALITVALAEKIKENVYLLPESIPF 480
QY 2110 LAELMEDECEVEEHOCQKTIQOLETVLGEPLQSYF 2144
DB 481 LAELMEDECEVEEHOCQKTIQOLETVLGEPLQSYF 515

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; RESULT 6
; US-60-167-217-22825
; Sequence 22825, Application US/60167217
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W. D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; FILE REFERENCE: CL000152

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; CURRENT APPLICATION NUMBER: US/60/167,217
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 23195
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 22825
; LENGTH: 2147
; TYPE: PRT
; ORGANISM: Drosophila
US-60-167-217-22825

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Query Match      18.6% Score 2012.5; DB 24; Length 2147;
Best Local Similarity 27.9%; Pred. No. 1.6e-150;
Matches 627; Conservative 423; Mismatches 911; Indels 289; Gaps 67;

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QY 14 POSDASLRDEVASLFLDPKEAATIDRTAFAGCTGLEELGIDPSFEQFEAPLFSQL 73
DB 66 POSSVTLADARSRAISILDPKEAATKDRRSIYEIGLQGLTDFNPAKFEQLTFDEA 125
QY 74 AKTERSVQTKAVNKOQDENISLFLHLSPEFLKPAQCKLEMLHFRHILNYODSLIA 133
DB 126 TLTTERSVLEPINKMLDAALAKELRLSLPLLRPAHMAFEWLLRRQVHEYNRSEYMA 185
QY 134 CVLPYHEIRIFVRVQLTKTNKSKHRMFWLPLPVKOSGVPPLAKGTILTHCYKDLGFMDFIC 193
DB 186 LILPYHEIMITVQIKYKTRLSRSGDQWYMLRPLORPGVPLAKTALINNAASNPAFLGFC 245
QY 194 SLVTKSVKFAVEYPOSSAQLNVLAFYASTIVSALVAEDVSDNIATAKPPYIOKGLKSS 253
DB 246 QSTQKAVK---ELGPRAHQLOAQINFAVTVVGAQLQAKPLQDMHITTLLESLRGLSD 302
QY 254 LPDYAAATYMIICQSVVYVNTFNVSLSAQIITLTKIPS-----LIKGLSCLIVLL 308
DB 303 NIDFMAAAYVIAQVLSRTKLSKVCNAL-----LERVNCPEERLHSESLLLVCIY 355
QY 309 QROKESISGKKPFPHLCWNPDLITLHGISEYDVSPLRYMLPLVYSII-----HHV 362
DB 356 GKQ-----QAALPAHF--KPE--TILNLVYKKWLISTLSLAKGNIAIOSICPLMTGAV 405
QY 363 TGEETEGMDGOYKRRHLEAITLISLKNLHLASLFEEYIS----- 406
DB 406 AAIRDDASSNCKFLDNLLESEVPMKPTAQOLINCFLDTRYVERAIDAPRPMETNSND 465
QY 407 -----YSSQEDMSKKVSLNEQPLRLLESKPRFLDVYVEHLEKIIDLKQELFPH 461
DB 466 DQTVIIDDDELETERKT--FOAWYSTYLEKERRRPEAFDLSEKALRSKSTSNROKAL 524
QY 462 QFV---SLTSGKTYQFLADSDPTSLMLSLNPLAPVRLANNH--LKKIMKTSKEGVDES 517
DB 525 KIALGFRLLNTDEKAKHAYE-----KLYHYSAWMKRSIAVOKLQNLNATKKRRRSYKL 577
QY 518 IKEAVLARIQDDNIDVLSAIS-AEIFKEHFSSEVTISNLNLFQRAELSKNGEWEVL 576
DB 578 LOECPLRINDSGAVVSTLLSLPTEELAEMLGPLPLAQIOTCHILLYRQOSKDEEMQV 637
QY 577 KIAAAILKEELISNDQLSNOVYVCLLPVYINDDTESAEKAIYLSKSGICSLPL 636
DB 638 PLAVRHLSALVSGSYD--TNLVLLALMPLLEPGCALAEHOKALRILIG--SDFVSKVPF 694
QY 637 LRGMEAELENVKSYPKGLKIGVANQKMIELLA--DNIMAGDS--SMLKMWEDLVSGEE 694
DB 695 LA--ELKYSNKSFDN-----VGEHRQHLIDITASSNOELSSOERALLDSVED---HGSEL 745
QY 695 SFNLKQKVTFAVILSVSCSSSLKETHPFAIRVFSLLQKRIKLESVITAVE-----I 749
DB 746 YLOKASQLT--HLLILLTAYAKRELQPRRESIMLEKIGLYSRLO--FRVYNGSQTOGCA 802
QY 750 PSEMHIELMDGIGIVELMAHVEELNSTORAAVDSVFLVSLKFLT-----YALKAKS 805
DB 803 PLQTLVDFLLT--VKNTKWT-----ALASTPNQMDELRLCLRLLEITCAOVFSKAOQ- 856
QY 806 FPKGDIMNPEQ-----LKEDSROYLHLIGLEWMLNGADAVHFRVLMKLIKVHLEDV 860

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XX Disclosure: Page 287-288; 348pp; English.

CC The sequence is that of a protein which can be used in the
 CC preparation of the recombinant breast cancer antigen, BRCA1, binding
 CC proteins BAR1, B123, BE2, BE14, BE31 or BE445, or a composition for the
 CC detection of a BAR1, B123, BE2, BE14, BE31 or BE445 nucleic acid
 CC sequence, specifically a wild type BAR1 composition for the detection
 CC or purification of BRCA1, useful to identify a patient having, or at
 CC risk of developing cancer. BAR1 can be used in the preparation of an
 CC anti-BAR1 antibody, and in the detection and purification of a BRCA1
 CC protein. BAR1, B123, BE2, BE14, BE31 or BE445 can be used in the
 CC identification of a binding protein agonist or antagonist that alters
 CC the binding of BAR1, B123, BE2, BE14, BE31 or BE445 to BRCA1 or the
 CC biological activity of the BRCA1-BAR1, B123, BE2, BE14, BE31 or BE445
 CC complex. The antibodies can be used to detect BAR1, B123, BE2, BE14,
 CC BE31 or BE445, a specific anti-BAR1 antibody can be used to identify
 CC a patient having or at risk of developing cancer.

XX Sequence 515 AA;

Query Match 23.9%; Score 2585; DB 19; Length 515;
 Best Local Similarity 99.0%; Pred. No. 3, 1e-180;
 Matches 510; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1630 NISKKKTVTRFLKLVDPDLAIYORKKKEGEQAINRQALYTLKLCNKGANPDPF 1689
 DB 1 NISKKKTVTRFLKLVDPDLAIYORKKKEGEQAINRQALYTLKLCNKGANPDPF 1689
 OY 1690 VPVYKTAVKLIAPRKEKKNVIGSALICIAEVSTLALALPOLPSMLTMTKATSE 1749
 DB 61 VPVYKTAVKLIAPRKEKKNVIGSALICIAEVSTLALALPOLPSMLTMTKATSE 1749
 OY 1750 LVSEVYLLSALAALQKRVETLPHFISPYLEGILSQVYHHEKIRSEKSAQANIRLTS 1809
 DB 121 LVSEVYLLSALAALQKRVETLPHFISPYLEGILSQVYHHEKIRSEKSAQANIRLTS 1809
 OY 1810 KKTATLAPRVILPAIKTKYKQIEKKNKKNHMPFMSILOEHGKMKKEELTSHQSOLTA 1869
 DB 181 KKTATLAPRVILPAIKTKYKQIEKKNKKNHMPFMSILOEHGKMKKEELTSHQSOLTA 1869
 OY 1870 FLEALDFRAOHSENDLEVEGKTEKNCITDCLVAVVYKLTSEVTPPLFEKLPDAKTTDAP 1929
 DB 241 FLEALDFRAOHSENDLEVEGKTEKNCITDCLVAVVYKLTSEVTPPLFEKLPDAKTTDAP 1929
 OY 1930 KDRLLTVYNADCLAEKLGKLFPLFAGHLVYKPRADTLXQVNIKTDEAFDSENDPEKCC 1989
 DB 301 KDRLLTVYNADCLAEKLGKLFPLFAGHLVYKPRADTLXQVNIKTDEAFDSENDPEKCC 1989
 OY 1990 LLLQFILNCLYKIFLPTOHFISKERAXALAMPVLDLENRLGEGEKFQERVTKHLIPCT 2049
 DB 361 LLLQFILNCLYKIFLPTOHFISKERAXALAMPVLDLENRLGEGEKFQERVTKHLIPCT 2049
 OY 2050 AOPSVAMADSLKPLNYQQLKTRDSSPVRFALITVALAEKLENTIVLLPSPIR 2109
 DB 421 AOPSVAMADSLKPLNYQQLKTRDSSPVRFALITVALAEKLENTIVLLPSPIR 2109
 OY 2110 LAELMEDECEVEHQCCKTQOLETVLGEPLQSYF 2144
 DB 481 LAELMEDECEVEHQCCKTQOLETVLGEPLQSYF 2144

RESULT 2

ID AAM19675 standard; Protein; 2932 AA.

XX AAM19675;

DT 20-AUG-1997 (first entry)

XX ATW mutant 2467del372.

KM ATM gene; ataxia-telangiectasia; progressive genetic disorder; antibody;
 KM central nervous system; immune system; chromosomal instability; therapy;
 KM cancer predisposition; radiation sensitivity; cell cycle abnormality;
 KM multi-system disease; autosomal recessive; cerebellar ataxia; cerebellum;
 KM general motor dysfunction; Purkinje cell; oculocutaneous telangiectasia;
 KM blood vessel; bulbar conjunctiva; facial skin; A-T; murelin.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Misc-difference 263 /note="encoded by CTT"
 FT Misc-difference 554 /note="encoded by ACG"
 FT Misc-difference 637 /note="encoded by CAA"
 FT Misc-difference 750 /note="encoded by AAC"
 FT Misc-difference 822..823 /note="site of 124 amino acid deletion"

XX MO9636691-A1.
 XX 21-NOV-1996.
 XX 16-MAY-1996; 96MO-US07025.
 XX 08-APR-1996; 96US-0629001.
 XX 16-MAY-1995; 95US-0441822.

XX (KOHN/) KOHN K I.
 XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX Shiloh Y;
 XX WPI; 1997-012070/01.
 XX N-PSDB; AAT68758.

XX New isolated ataxia-telangiectasia gene - used to develop prods. for
 XX the study, diagnosis and treatment of ataxia-telangiectasia.

XX Claim 5; Page -; 153pp; English.

XX AAM19648-W19702 represent mutations of the ATM gene of the invention
 CC (see AAM06234 for wild type sequence). The ATM gene of the invention, is
 CC located in the human genome at chromosome segment 11q22-23.
 CC Ataxia-telangiectasia (A-T) is caused by mutations, insertions, or
 CC deletions (such as represented by this sequence) in the coding region of
 CC the ATM gene. A-T is a progressive genetic disorder affecting the central
 CC nervous and immune systems. A-T involves chromosomal instability, cancer
 CC predisposition, radiation sensitivity, and cell cycle abnormalities. A-T
 CC is a multi-system disease inherited in an autosomal recessive manner.
 CC The wild type gene, can be used in methods for detecting carriers of a
 CC defective gene that causes A-T. The gene can also be used to generate
 CC antibodies. The methods and antibodies can be used in the study,
 CC diagnosis and therapy of A-T.

XX Sequence 2932 AA;

Query Match 2.5%; Score 273; DB 18; Length 2932;
 Best Local Similarity 18.6%; Pred. No. 2, 8e-10;
 Matches 411; Conservative 354; Mismatches 777; Indels 662; Gaps 105;

OY 236 DNIIAKLPYIOG---LKSSLPDYRAATYMIICQISVYKMENTFVNSLSAQITK--- 288
 DB 58 dafvfrlqkylqketeclrlakpnvsast---qasrqqkmg---lslvkyfikcanr 110
 OY 289 -----TLTKIPSLRKD-----GLSCLIVLQROKESLGKRFPHLCNP----- 328
 DB 111 repvrlkgeellnyindvkvkdsngaiygadcsnllk-----dlsvrky--wcelsqgw 164
 OY 329 -DLITLHGISEFTYDVSPILRYMLPH-----LVVSIHHTVG---EETEGMDGOIYKRH 378

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2001, 15:12:03 ; Search time 34.51 Seconds

(without alignments)
3766.382 Million cell updates/sec

Title: US-09-603-665-5

Perfect score: 10807

Sequence: 1 MSLAQQLRLALPQSDASL.....CKTIQQLFTVGEPIQSYF 2144

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : A.Geneseq.0601.*

- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.*
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- 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2585	23.9	515	19	AAW54099
2	273	2.5	2932	18	AAW19675
3	272.5	2.5	2954	20	AAW01632
4	271.5	2.5	3055	18	AAW19697
5	270.5	2.5	2989	18	AAW19688
6	262.5	2.4	3059	18	AAW19696
7	262	2.4	2998	18	AAW19691
8	262	2.4	3046	18	AAW19690
9	262	2.4	3053	18	AAW19694
10	262	2.4	3054	18	AAW19695
11	262	2.4	3055	18	AAW19693

12	262	2.4	3056	18	AAW19733	Cell cycle checkpo
13	262	2.4	3056	18	AAW19698	ATM mutant E2904G.
14	262	2.4	3056	18	AAW19699	ATM mutant Leu43Pr
15	262	2.4	3056	19	AAW37133	Ataxia-telangiecta
16	262	2.4	3056	20	AAW84269	Human ataxia telan
17	261	2.4	2075	18	AAW19662	ATM mutant 6199del
18	261	2.4	2193	18	AAW19660	ATM mutant 6573del
19	261	2.4	2415	18	AAW19686	ATM mutant 7240del
20	261	2.4	2507	18	AAW19659	ATM mutant 7517del
21	261	2.4	2545	18	AAW19657	ATM mutant 7630del
22	261	2.4	2598	18	AAW19656	ATM mutant 7789del
23	261	2.4	2652	18	AAW19655	ATM mutant 7883del
24	261	2.4	2713	18	AAW19654	ATM mutant C8140T.
25	261	2.4	2759	18	AAW19652	ATM mutant 8269del
26	261	2.4	2766	18	AAW19651	ATM mutant 8283del
27	261	2.4	2768	18	AAW19650	ATM mutant 8283del
28	261	2.4	2987	18	AAW19649	ATM mutant 8307A.
29	261	2.4	3003	18	AAW19648	ATM mutant 8946Ins
30	261	2.4	3005	18	AAW19653	ATM mutant 7630del
31	261	2.4	3005	18	AAW19648	ATM mutant 8269del
32	261	2.4	3021	18	AAW19661	ATM mutant 9001del
33	261	2.4	3054	18	AAW19702	ATM mutant 6348del
34	261	2.4	3056	18	AAW06234	ATM mutant 7278del
35	261	2.4	3056	18	AAW07655	ATM protein. Homo
36	261	2.4	3085	18	AAW07655	Ataxia-telangiecta
37	260.5	2.4	3057	22	AAW19701	ATM mutant G9170C.
38	260	2.4	2998	18	AAW19673	Human ATM protein.
39	259	2.4	3066	18	AAW36178	ATM mutant 3403del
40	258	2.4	3026	18	AAW19676	Murine Ataxia-tela
41	255.5	2.4	3433	18	AAW22017	ATM mutant 2377del
42	255	2.4	3056	22	AAW19654	Ulrophin. Homo sa
43	254.5	2.4	2825	21	AAW19685	Human ATM protein.
44	254.5	2.4	2837	21	AAW30671	Arabidopsis thalia
45	254.5	2.4	2895	21	AAW30669	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAW54099

ID AAW54099 standard; Protein: 515 AA.

AC AAW54099;

XX

XX 28-SEP-1998 (first entry)

DT

XX Homo sapiens BAP28 sequence.

DE

XX

KW BARD1; ring protein; BRCAL; breast cancer; risk; diagnosis.

XX

OS Homo sapiens.

XX

FN W09812327-A2.

XX

PD 26-MAR-1998.

XX

PE 19-SEP-1997; 97WO-US16842.

XX

PR 04-APR-1997; 97US-0042985.

PR 20-SEP-1996; 96US-0025296.

PR 03-APR-1997; 97US-0042611.

XX

PA (TEXA) UNIT TEXAS SYSTEM.

PI

PI Baer R. Bowcock AM;

XX

XX WPI; 1998-230317/20.

DR

DR N-PSDB; AAV24135.

XX

PT DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - which

PT as breast cancer antigen, BRCAL, binding proteins are useful to

PT identify patient having or at risk of developing cancer